

SEQUENCE LISTING

<110> Gressel, Jonathan
Eyal, Yoram
Fluhr, Robert

<120> RHAMNOSYL-TRANSFERASE GENE AND USES THEREOF

<130> 01/22289

<140> US 09/889,738

<141> 2000-01-20

<150> IL 128193

<151> 1999-01-20

<150> PCT/IL00/00038

<151> 2000-01-20

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 8

<212> PRT

<213> Citrus X paradisi

<400> 1

Asn Tyr Phe Leu His Leu Thr Ala
1 5

<210> 2

<211> 3

<212> PRT

<213> Citrus X paradisi

<400> 2

Tyr Pro Phe
1

<210> 3

<211> 7

<212> PRT

<213> Citrus X paradisi

<400> 3

Ile Ala Ala Ile Leu Phe Leu
1 5

<210> 4

<211> 8

<212> PRT

<213> Citrus X paradisi

<400> 4

Tyr Phe Pro Ser Leu Met Gly Asn
1 5

<210> 5

<211> 8
 <212> PRT
 <213> Citrus X paradisi
 <400> 5

Glu Lys Met Thr Ile Glu Glu Ala
 1 5

<210> 6
 <211> 4
 <212> PRT
 <213> Citrus X paradisi
 <400> 6

Leu Phe Gln Pro
 1

<210> 7
 <211> 14
 <212> PRT
 <213> Citrus X paradisi
 <400> 7

Val Val Asp Asn Gly Met Gly Met Val Val Pro Arg Asp Lys
 1 5 10

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> Modified base : Inosine

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> Modified base : Inosine

<400> 8
 gayaayggna tgggnatggt

20

<210> 9
 <211> 7
 <212> PRT
 <213> Citrus X paradisi
 <400> 9

Asp Asn Gly Met Gly Met Val
 1 5

<210> 10

<211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> Modified base: Inosine

<400> 10
 garaaratga cnathgarga rgc

23

<210> 11
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> Modified base : Inosine

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> Modified base : Inosine

<220>
 <221> misc_feature
 <222> (21)..(21)
 <223> Modified base : Inosine

<400> 11
 aaytayttyc tncayctnac ngc

23

<210> 12
 <211> 8
 <212> PRT
 <213> Citrus X paradisi

<400> 12

Asn Tyr Phe Leu His Leu Thr Ala
 1 5

<210> 13
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 13
 gttttccag tcacgacgtt tttttttttt ttt

33

<210> 14
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 14
 gttttcccag tcacgacg 18

<210> 15
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 15
 catgcccata ccattgtc 18

<210> 16
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 16
 gacaatggta tgggcatg 18

<210> 17
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 17
 cctcaaccac cgagccccaa ccac 24

<210> 18
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 18
 catctagaat ggataccaag catcaag 27

<210> 19
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 19

caggatcctt attcagattt cttgacaag

29

<210> 20

<211> 1359

<212> DNA

<213> Citrus X paradisi

<400> 20

atggatacca agcatcaaga taagccaagc attctcatgt taccatggct agctcatggg	60
cacatagctc cacaccttga acttgccaag aagctttcac agaaaaactt ccacatatat	120
ttctgctcta ctcccaacaa tctacaatcc ttcggcagaa atgttgaaaa aaacttctca	180
tcttcaatac aactcataga actgcaactt cccaatacat tccctgaact tccttcacaa	240
aatcagacca caaaaaacct tcctcccat cttatttata ctctcgtggg agcatttgaa	300
gacgcaaac ctgctttttg caacatcttg gagacgctta aaccaaccct tgttatgtat	360
gatttgttcc aaccgatggc ggcggaggca gcttaccagt atgacatagc tgctattttg	420
ttcttaccct tatctgcagt agcctgctct ttcttgctgc acaatatcgt aaatcccagc	480
ctgaaatacc ctttctttga atctgattac caagatagag aaagcaagaa catcaattac	540
ttcctgcatc ttactgcaa tggcacctta aacaaagaca ggttcttaaa agctttcgaa	600
ctatcttgca aatttggtgt catcaaaaca tcaagagaga ttgaatcaa gtacttggat	660
tattttcctt ctttaatggg aaatgaaata attccagtag ggcctctaata ccaagaacct	720
accttcaagg tagatgatac aaagatcatg gactggctga gccaaaagga gcctcgttca	780
gtcgtgtatg catccttttg cagtgcgtac ttcccttcca cggatgaaat acatgacata	840
gctattgggt tattgctcac cgagggttaatt ttatatggg ctttcagatt acatcctgat	900
gagaaaatga cgatagagga agcactgcct cagggctttg ctgaggagat tgaaagggaat	960
aataagggaa tgatagtaca aggttggggt ccgcaggcta aaattttaag gcatggaagc	1020
atcggcggat ttttgagtca ttgtgggttg ggctcgggtg ttgaggggat ggttttcggg	1080
gtaccaatca taggtgtgcc aatggcatat gagcagccaa gcaatgccaa ggtggtggtt	1140
gacaatggta tgggcatggt cgttccaaga gataagatca atcaaagact tggaggagag	1200
gaggtggcga gggtcattaa acatgtttgt ctgcaagaag aagcgaagca aataagaaga	1260
aaagctaata aaattagtga gagtatgaag aagatagggg acgcacagat gagtgtggtg	1320
gtggagaaac tgctgcagct tgtcaagaaa tctgaataa	1359

<210> 21

<211> 452

<212> PRT

<213> Citrus X paradisi

<400> 21

Met	Asp	Thr	Lys	His	Gln	Asp	Lys	Pro	Ser	Ile	Leu	Met	Leu	Pro	Trp
1				5				10						15	

Leu Ala His Gly His Ile Ala Pro His Leu Glu Leu Ala Lys Lys Leu
20 25 30

Ser Gln Lys Asn Phe His Ile Tyr Phe Cys Ser Thr Pro Asn Asn Leu
35 40 45

Gln Ser Phe Gly Arg Asn Val Glu Lys Asn Phe Ser Ser Ser Ile Gln
50 55 60

Leu Ile Glu Leu Gln Leu Pro Asn Thr Phe Pro Glu Leu Pro Ser Gln
65 70 75 80

Asn Gln Thr Thr Lys Asn Leu Pro Pro His Leu Ile Tyr Thr Leu Val
85 90 95

Gly Ala Phe Glu Asp Ala Lys Pro Ala Phe Cys Asn Ile Leu Glu Thr
100 105 110

Leu Lys Pro Thr Leu Val Met Tyr Asp Leu Phe Gln Pro Met Ala Ala
115 120 125

Glu Ala Ala Tyr Gln Tyr Asp Ile Ala Ala Ile Leu Phe Leu Pro Leu
130 135 140

Ser Ala Val Ala Cys Ser Phe Leu Leu His Asn Ile Val Asn Pro Ser
145 150 155 160

Leu Lys Tyr Pro Phe Phe Glu Ser Asp Tyr Gln Asp Arg Glu Ser Lys
165 170 175

Asn Ile Asn Tyr Phe Leu His Leu Thr Ala Asn Gly Thr Leu Asn Lys
180 185 190

Asp Arg Phe Leu Lys Ala Phe Glu Leu Ser Cys Lys Phe Val Phe Ile
195 200 205

Lys Thr Ser Arg Glu Ile Glu Ser Lys Tyr Leu Asp Tyr Phe Pro Ser
210 215 220

Leu Met Gly Asn Glu Ile Ile Pro Val Gly Pro Leu Ile Gln Glu Pro
225 230 235 240

Thr Phe Lys Val Asp Asp Thr Lys Ile Met Asp Trp Leu Ser Gln Lys
245 250 255

Glu Pro Arg Ser Val Val Tyr Ala Ser Phe Gly Ser Glu Tyr Phe Pro
260 265 270

Ser Thr Asp Glu Ile His Asp Ile Ala Ile Gly Leu Leu Leu Thr Glu
275 280 285

Val Asn Phe Ile Trp Ala Phe Arg Leu His Pro Asp Glu Lys Met Thr
 290 295 300

Ile Glu Glu Ala Leu Pro Gln Gly Phe Ala Glu Glu Ile Glu Arg Asn
 305 310 315 320

Asn Lys Gly Met Ile Val Gln Gly Trp Val Pro Gln Ala Lys Ile Leu
 325 330 335

Arg His Gly Ser Ile Gly Gly Phe Leu Ser His Cys Gly Trp Gly Ser
 340 345 350

Val Val Glu Gly Met Val Phe Gly Val Pro Ile Ile Gly Val Pro Met
 355 360 365

Ala Tyr Glu Gln Pro Ser Asn Ala Lys Val Val Val Asp Asn Gly Met
 370 375 380

Gly Met Val Val Pro Arg Asp Lys Ile Asn Gln Arg Leu Gly Gly Glu
 385 390 395 400

Glu Val Ala Arg Val Ile Lys His Val Val Leu Gln Glu Glu Ala Lys
 405 410 415

Gln Ile Arg Arg Lys Ala Asn Glu Ile Ser Glu Ser Met Lys Lys Ile
 420 425 430

Gly Asp Ala Gln Met Ser Val Val Val Glu Lys Leu Leu Gln Leu Val
 435 440 445

Lys Lys Ser Glu
 450